

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 09/890,729A
Source: 1Fw/6
Date Processed by STIC: 5/23/05

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IFW16

RAW SEQUENCE LISTING

DATE: 05/23/2005

PATENT APPLICATION: US/09/890,729A

TIME: 09:28:25

Input Set : A:\A-579B.ST25.txt

Output Set: N:\CRF4\05232005\I890729A.raw

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3 <110> APPLICANT: YOSHINAGA, STEVEN KIYOSHI
5 <120> TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE.
7 <130> FILE REFERENCE: A-579B
9 <140> CURRENT APPLICATION NUMBER: US 09/890,729A
10 <141> CURRENT FILING DATE: 2001-08-03
12 <150> PRIOR APPLICATION NUMBER: PCT US00/01871
13 <151> PRIOR FILING DATE: 2000-01-27
15 <150> PRIOR APPLICATION NUMBER: 09/264,527
16 <151> PRIOR FILING DATE: 1999-03-08
18 <150> PRIOR APPLICATION NUMBER: 09/244,448
19 <151> PRIOR FILING DATE: 1999-02-03
21 <160> NUMBER OF SEQ ID NOS: 37
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 600
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus musculus
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(600)
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38 1          5          10          15
40 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca      96
41 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
42          20          25          30
44 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc      144
45 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
46          35          40          45
48 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa      192
49 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50          50          55          60
52 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca      240
53 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
54 65          70          75          80
56 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta      288
57 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
58          85          90          95
60 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
61 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
62          100          105          110
64 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat      384

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65 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
66      115      120      125
68 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta      432
69 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
70      130      135      140
72 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata      480
73 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
74 145      150      155      160
76 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac      528
77 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
78      165      170      175
80 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag      576
81 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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86      195      200
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90 <211> LENGTH: 200
91 <212> TYPE: PRT
92 <213> ORGANISM: Mus musculus
94 <400> SEQUENCE: 2
96 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
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100 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
101      20      25      30
104 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
105      35      40      45
108 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
109      50      55      60
112 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
113 65      70      75      80
116 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
117      85      90      95
120 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
121      100      105      110
124 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
125      115      120      125
128 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
129      130      135      140
132 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
133 145      150      155      160
136 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
137      165      170      175
140 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
141      180      185      190
144 Ser Arg Leu Ala Gly Val Thr Ser
145      195      200
148 <210> SEQ ID NO: 3

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Input Set : A:\A-579B.ST25.txt

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150 <212> TYPE: PRT

151 <213> ORGANISM: Mus musculus

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163 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val

164 35 40 45

167 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu

168 50 55 60

171 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro

172 65 70 75 80

175 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu

176 85 90 95

179 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser

180 100 105 110

183 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr

184 115 120 125

187 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu

188 130 135 140

191 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile

192 145 150 155 160

195 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp

196 165 170 175

199 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys

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203 Ser Arg Leu Ala Gly Val Thr Ser

204 195 200

207 <210> SEQ ID NO: 4

208 <211> LENGTH: 218

209 <212> TYPE: PRT

210 <213> ORGANISM: Mus musculus

212 <400> SEQUENCE: 4

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215 1 5 10 15

218 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val

219 20 25 30

222 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu

223 35 40 45

226 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val

227 50 55 60

230 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg

231 65 70 75 80

234 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val

235 85 90 95

238 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe

239 100 105 110

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242 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
243      115      120      125
246 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
247      130      135      140
250 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Ala Gly Val
251 145      150      155      160
254 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
255      165      170      175
258 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
259      180      185      190
262 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
263      195      200      205
266 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
267      210      215
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271 <211> LENGTH: 44
272 <212> TYPE: PRT
273 <213> ORGANISM: Artificial sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Synthetic
278 <400> SEQUENCE: 5
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281 1      5      10      15
284 Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
285      20      25      30
288 Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
289      35      40
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293 <211> LENGTH: 966
294 <212> TYPE: DNA
295 <213> ORGANISM: Mus musculus
298 <220> FEATURE:
299 <221> NAME/KEY: CDS
300 <222> LOCATION: (1)..(966)
302 <400> SEQUENCE: 6
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305 1      5      10      15
307 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
308 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
309      20      25      30
311 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act      144
312 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
313      35      40      45
315 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac      192
316 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
317      50      55      60
319 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa      240
320 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln

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321 65          70          75          80
323 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct      288
324 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
325          85          90          95
327 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc      336
328 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
329          100          105          110
331 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc      384
332 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
333          115          120          125
335 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca      432
336 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
337          130          135          140
339 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg      480
340 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
341          145          150          155          160
343 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac      528
344 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
345          165          170          175
347 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca      576
348 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
349          180          185          190
351 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac      624
352 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
353          195          200          205
355 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat      672
356 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
357          210          215          220
359 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt      720
360 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
361          225          230          235          240
363 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att      768
364 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
365          245          250          255
367 agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa      816
368 Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
369          260          265          270
371 acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg      864
372 Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
373          275          280          285
375 gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc      912
376 Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
377          290          295          300
379 cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac      960
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384 His Ala
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VERIFICATION SUMMARY

DATE: 05/23/2005

PATENT APPLICATION: US/09/890,729A

TIME: 09:28:26

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